AMENDMENTS TO THE CLAIMS

Please amend claim 1, add claims 83-114, and cancel claims 2-82, without prejudice or disclaimer.

The listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Currently Amended) A method of inferring a trait of, with a predetermined level of confidence, proportional ancestry of at least two ancestral groups of an individual by identification of a population structure comprising:

a) identifying a first population of single polynucleotide polymorphisms (SNPs) having a frequency differential (δ) > 0.4 between one or more pairs of population groups;

b) contacting a parental sample nucleic acid with one or more hybridizing nucleic acids corresponding the first population of SNPs;

c) selecting SNPs hybridizing in step (b) to generate a second population of SNPs which have a minor allele frequency > 1% and a δ > 0.4 for at least one pair of the at least two population groups, wherein at least one of the second population of SNPs is a SNP which may be correlated with but not linked to a gene-linked trait, and wherein the at least one SNP of the second population of SNPs is not located within a gene encoding region;

d) contacting a sample comprising nucleic acid molecules of a non-parental individual with the hybridizing oligonucleotides second population of SNPs, wherein the contacting detects nucleotide occurrences of single nucleotide polymorphisms (SNPs) in a panel of ancestry informative markers (AIMs), wherein the panel comprises at least about ten AIMs selected from SEQ ID NOs: 1 to 311, wherein the AIMS second population of SNPs are indicative of a population structure, and wherein the population structure is correlated with a trait of the non-parental individual, and wherein the panel comprises at least one AIM that is not linked to a gene linked to the trait; and

e) determining the nucleotide occurrences of the second population of SNPs in the sample from the non-parental individual; and

f) identifying the population structure indicated by the nucleotide occurrences ~~of the~~ ~~AIMs detect in~~ determined for the non-parental individual ~~of step(a)~~, wherein identifying the population structure infers the ~~trait~~ proportional ancestry of the non-parental individual.

2-82. (Canceled)

83. (New) The method of claim 1, wherein the first population SNPs are identified from a database *in silico*.

84. (New) The method of claim 1, wherein the identifying step (a) comprises demonstrating a δ > 0.4 between any two of four intercontinental or intracontinental population groups or determining an Fst >0.4 at an average spacing of about 2-3 cM between any two of four intercontinental or intracontinental population groups.

85. (New) The method of claim 1, wherein the one or more pairs is from at least two intercontinental or intracontinental population groups.

86. (New) The method of claim 84, wherein the parental sample is from a human individual determined to be a Sub-Saharan African, an IndoEuropean, an East Asian, a Native American, a Northern European, a Continental European, an Iberian, a Northeastern European, a Middle Eastern European, a South Asian European, or a Southeastern European.

87. (New) The method of claim 1, wherein the sample of step (d) is contacted with at least 200 second population SNPs.

88. (New) The method of claim 1, wherein the sample of step (d) is contacted with at least 100 second population SNPs.

89. (New) The method of claim 1, wherein the sample of step (d) is contacted with at least 20 second population SNPs.

90. (New) The method of claim 1, wherein the trait comprises biogeographical ancestry (BGA).

91. (New) The method of claim 1, wherein proportional ancestry is determined by employing an algorithm which maximizes a cumulative δ value between, and minimizes a difference in cumulative δ value within, each of the one or more pairs of the population groups.

92. (New) The method of claim 91, wherein the algorithm inverts population specific allele frequencies, thereby obtaining a likelihood estimate, or a likelihood based estimate, of proportional ancestry corresponding to a multilocus genotype.

93. (New) The method of claim 92, wherein the likelihood estimate is measured for at least three of the intercontinental or intracontinental population groups simultaneously.

94. (New) The method of claim 93, wherein the estimate is repeated for all possible intercontinental or intracontinental population groups.

95. (New) The method of claim 1, wherein the intercontinental or intracontinental population groups are delimited as Sub-Saharan African, IndoEuropean, East Asian, Native American, Northern European, Continental European, Iberian, Northeastern European, Middle Eastern European, South Asian European, or Southeastern European.

96. (New) The method of claim 90, wherein the BGA comprises a proportion of Sub-Saharan African, IndoEuropean, East Asian, Native American, Northern European, Continental European, Iberian, Northeastern European, Middle Eastern European, South Asian European, or Southeastern European ancestral groups, or a combination thereof.

97. (New) The method of claim 96, wherein the proportional ancestry comprises proportions of at least two ancestral groups.

98. (New) The method of clam 97, further comprising performing a likelihood determination for affiliation with each of a sub-Saharan African ancestral group, a Native American ancestral group, an IndoEuropean ancestral group, and an East Asian ancestral group;

        selecting three ancestral groups having a greatest likelihood value;

        determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with the nucleotide occurrences of the SNPs detected in the non parental individual is identified; and

        identifying a single proportional combination of maximum likelihood.

99. (New) The method of claim 97, further comprising performing six two-way comparisons comprising likelihood determinations for affiliation between each group with each other group;

        selecting three ancestral groups having a greatest likelihood value;

        determining a likelihood of all possible proportional affiliations among three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with the nucleotide occurrences of the SNPs detected in the non-parental individual is identified; and

        identifying a single proportional combination of maximum likelihood.

100. (New) The method of claim 97, further comprising performing three three-way comparisons among the groups;

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determining a likelihood of all possible proportional affiliations among three ancestral

groups having the greatest likelihood value, whereby a population structure that correlates with

the nucleotide occurrences of the SNPs detected in the non-parental individual is identified; and

identifying a single proportional combination of maximum likelihood.

101. (New) The method of claim 97, further comprising performing six two-way comparisons,

the three three-way comparisons, or one four-way comparison among four ancestral groups;

determining a likelihood of all possible proportional affiliations among four ancestral

groups having the greatest likelihood value, whereby a population structure that correlates with

the nucleotide occurrences of the SNPs detected in the non-parental individual is identified; and

identifying a single proportional combination of maximum likelihood.

102. (New) The method of clam 99, further comprising generating a graphical representation of

the comparison of the three ancestral groups, the graphical representation comprising a triangle

with each ancestral group independently represented by a vertex of the triangle, wherein the

maximum likelihood value of proportional affiliation for a non-parental individual comprises a

point within the triangle.

103. (New) The method of clam 102, wherein the graphical representation further comprises a

confidence contour indicating a level of confidence associated with estimating the proportional

ancestry.

104. (New) The method of claim 97, further comprising identifying an ethnicity of the non-

parental individual, which comprises identifying a subpopulation structure of the population

structure indicated by the nucleotide occurrences of the SNPs detected in the non-parental

individual, wherein the SNPs are further indicative of a sub-population structure, and wherein

the sub-population structure infers ethnicity of the non-parental individual.

105. (New) The method of claim 104, wherein the ancestral group is IndoEuropean, and wherein the ethnicity comprises Northern European or Mediterranean.

106. (New) The method of claim 97, further comprising generating an ancestral map of the world, wherein locations of populations having a proportional ancestry corresponding to the proportional ancestry of the individual are indicated on the ancestral map.

107. (New) The method of claim 97, wherein identifying a population structure indicated by the nucleotide occurrences of the SNPs detected in the non-parental individual comprises comparing the nucleotide occurrences of the SNPs detected in the non parental individual with known proportional ancestries corresponding to nucleotide occurrences of SNPs indicative of BGA.

108. (New) The method of claim 107, wherein the known proportional ancestries corresponding to nucleotide occurrences of SNPs indicative of BGA are contained in a database.

109. (New) The method of claim 108, wherein the comparing is performed using a computer.

110. (New) The method of claim 107, wherein each of the known proportional ancestries corresponding to nucleotide occurrences of SNPs indicative of BGA further comprises at least one photograph of a person from whom the known proportional ancestry was determined.

111. (New) The method of claim 110, wherein the at least one photograph comprises a digital photograph.

112. (New) The method of claim 111, wherein digital information comprising the digital photograph is contained in a database.

113. (New) The method of claim 112, wherein the digital information in the database is associated with the known proportional ancestry corresponding to nucleotide occurrences of SNPs indicative of BGA of the person in the photograph.

114. (New) The method of claim 108, further comprising identifying at least one photograph of a person having a proportional ancestry corresponding to the proportional ancestry of a test individual.

115. (New) The method of claim 114, wherein identifying the photograph comprises scanning a database comprising a plurality of files, each file comprising digital information corresponding to a digital photograph of a person having a known proportional ancestry, and identifying at least one photograph of a person having nucleotide occurrences of SNPs indicative of BGA that correspond to the nucleotide occurrences of SNPs indicative of BGA of the test individual.